



PCT

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## RAW SEQUENCE LISTING

DATE: 12/16/2002

PATENT APPLICATION: US/09/762,527A

TIME: 13:33:02

Input Set : A:\PF-0576 USN SEQUENCE LISTING.txt

Output Set: N:\CRF4\12162002\I762527A.raw

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5 <110> APPLICANT: INCYTE PHARMACEUTICALS, INC.
6     HILLMAN, Jennifer L.
7     YUE, Henry
8     CORLEY, Neil C.
9     GUEGLER, Karl J.
10    PATTERSON, Chandra
12 <120> TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS
14 <130> FILE REFERENCE: PF-0576 PCT
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/762,527A
C--> 17 <141> CURRENT FILING DATE: 2002-04-17
19 <150> PRIOR APPLICATION NUMBER: 09/131,648
20 <151> PRIOR FILING DATE: 1998-08-10
22 <160> NUMBER OF SEQ ID NOS: 5
24 <170> SOFTWARE: PERL Program
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 336
29 <212> TYPE: PRT
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: misc_feature
34 <223> OTHER INFORMATION: Incyte Clone No: 2635136
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38   1           5           10           15
39 Ser Trp Ser Cys Pro Thr Val Met Ser Pro Gly Glu Lys Leu Asp
40           20           25           30
41 Pro Ile Pro Asp Ser Phe Ile Leu Gln Pro Pro Val Phe His Pro
42           35           40           45
43 Val Val Pro Tyr Val Thr Thr Ile Phe Gly Gly Leu His Ala Gly
44           50           55           60
45 Lys Met Val Met Leu Gln Gly Val Val Pro Leu Asp Ala His Arg
46           65           70           75
47 Phe Gln Val Asp Phe Gln Cys Gly Cys Ser Leu Cys Pro Arg Pro
48           80           85           90
49 Asp Ile Ala Phe His Phe Asn Pro Arg Phe His Thr Thr Lys Pro
50           95          100          105
51 His Val Ile Cys Asn Thr Leu His Gly Gly Arg Trp Gln Arg Glu
52          110          115          120
53 Ala Arg Trp Pro His Leu Ala Leu Arg Arg Gly Ser Ser Phe Leu
54          125          130          135
55 Ile Leu Phe Leu Phe Gly Asn Glu Glu Val Lys Val Ser Val Asn
56          140          145          150
57 Gly Gln His Phe Leu His Phe Arg Tyr Arg Leu Pro Leu Ser His

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58          155          160          165
59 Val Asp Thr Leu Gly Ile Phe Gly Asp Ile Leu Val Glu Ala Val
60          170          175          180
61 Gly Phe Leu Asn Ile Asn Pro Phe Val Glu Gly Ser Arg Glu Tyr
62          185          190          195
63 Pro Ala Gly His Pro Phe Leu Leu Met Ser Pro Arg Leu Glu Val
64          200          205          210
65 Pro Cys Ser His Ala Leu Pro Gln Gly Leu Ser Pro Gly Gln Val
66          215          220          225
67 Ile Ile Val Arg Gly Leu Val Leu Gln Glu Pro Lys His Phe Thr
68          230          235          240
69 Val Ser Leu Arg Asp Gln Ala Ala His Ala Pro Val Thr Leu Arg
70          245          250          255
71 Ala Ser Phe Ala Asp Arg Thr Leu Ala Trp Ile Ser Arg Trp Gly
72          260          265          270
73 Gln Lys Lys Leu Ile Ser Ala Pro Phe Leu Phe Tyr Pro Gln Arg
74          275          280          285
75 Phe Phe Glu Val Leu Leu Leu Phe Gln Glu Gly Gly Leu Lys Leu
76          290          295          300
77 Ala Leu Asn Gly Gln Gly Leu Gly Ala Thr Ser Met Asn Gln Gln
78          305          310          315
79 Ala Leu Glu Gln Leu Arg Glu Leu Arg Ile Ser Gly Ser Val Gln
80          320          325          330
81 Leu Tyr Cys Val His Ser
82          335
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88 <211> LENGTH: 708
89 <212> TYPE: PRT
90 <213> ORGANISM: Homo sapiens
92 <220> FEATURE:
93 <221> NAME/KEY: misc feature
94 <223> OTHER INFORMATION: Incyte Clone No: 2687731
96 <400> SEQUENCE: 2
97 Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala
98   1          5          10          15
99 Ile Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro
100          20          25          30
101 Arg Leu Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser
102          35          40          45
103 Ile Tyr Met Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu
104          50          55          60
105 Leu Thr Phe Pro Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu
106          65          70          75
107 Leu Gln Thr Asn Asn Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe
108          80          85          90
109 Pro Val Asn Leu Thr Gly Leu Asp Leu Ser Gln Asn Asn Leu Ser
110          95          100          105
111 Ser Val Thr Asn Ile Asn Val Lys Lys Met Pro Gln Leu Leu Ser
112          110          115          120

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113 Val Tyr Leu Glu Glu Asn Lys Leu Thr Glu Leu Pro Glu Lys Cys
114                               125                               130                               135
115 Leu Ser Glu Leu Ser Asn Leu Gln Glu Leu Tyr Ile Asn His Asn
116                               140                               145                               150
117 Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe Ile Gly Leu His Asn
118                               155                               160                               165
119 Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu Gln Met Ile Asn
120                               170                               175                               180
121 Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile Leu Met Ile
122                               185                               190                               195
123 Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe Lys Pro
124                               200                               205                               210
125 Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu Thr
126                               215                               220                               225
127 Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
128                               230                               235                               240
129 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala
130                               245                               250                               255
131 Leu Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn
132                               260                               265                               270
133 Pro Ile Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His
134                               275                               280                               285
135 Leu Lys Glu Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile
136                               290                               295                               300
137 Asp Ser Leu Ala Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu
138                               305                               310                               315
139 Ala Thr Asn Asn Pro Arg Leu Ser Tyr Ile His Pro Asn Ala Phe
140                               320                               325                               330
141 Phe Arg Leu Pro Lys Leu Glu Ser Leu Met Leu Asn Ser Asn Ala
142                               335                               340                               345
143 Leu Ser Ala Leu Tyr His Gly Thr Ile Glu Ser Leu Pro Asn Leu
144                               350                               355                               360
145 Lys Glu Ile Ser Ile His Ser Asn Pro Ile Arg Cys Asp Cys Val
146                               365                               370                               375
147 Ile Arg Trp Met Asn Met Asn Lys Thr Asn Ile Arg Phe Met Glu
148                               380                               385                               390
149 Pro Asp Ser Leu Phe Cys Val Asp Pro Pro Glu Phe Gln Gly Gln
150                               395                               400                               405
151 Asn Val Arg Gln Val His Phe Arg Asp Met Met Glu Ile Cys Leu
152                               410                               415                               420
153 Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu Asn Val Glu
154                               425                               430                               435
155 Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala Glu Pro
156                               440                               445                               450
157 Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu Leu
158                               455                               460                               465
159 Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr
160                               470                               475                               480
161 Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr

```

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162                               485                               490                               495
163 Cys Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met
164                               500                               505                               510
165 Ile Lys Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu
166                               515                               520                               525
167 Asn Ile Lys Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser
168                               530                               535                               540
169 Trp Lys Ala Ser Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr
170                               545                               550                               555
171 Ala Phe Val Lys Thr Glu Asn Ser His Ala Ala Gln Ser Ala Arg
172                               560                               565                               570
173 Ile Pro Ser Asp Val Lys Val Tyr Asn Leu Thr His Leu Asn Pro
174                               575                               580                               585
175 Ser Thr Glu Tyr Lys Ile Cys Ile Asp Ile Pro Thr Ile Tyr Gln
176                               590                               595                               600
177 Lys Asn Arg Lys Lys Cys Val Asn Val Thr Thr Lys Gly Leu His
178                               605                               610                               615
179 Pro Asp Gln Lys Glu Tyr Glu Lys Asn Asn Thr Thr Thr Leu Met
180                               620                               625                               630
181 Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile Gly Val Ile Cys Leu
182                               635                               640                               645
183 Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp Gly Gly His Ser
184                               650                               655                               660
185 Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala Leu Gly Glu
186                               665                               670                               675
187 Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys Glu Lys
188                               680                               685                               690
189 Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro Thr
190                               695                               700                               705

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191 Asn Met Ser

196 &lt;210&gt; SEQ ID NO: 3

197 &lt;211&gt; LENGTH: 1643

198 &lt;212&gt; TYPE: DNA

199 &lt;213&gt; ORGANISM: Homo sapiens

201 &lt;220&gt; FEATURE:

202 &lt;221&gt; NAME/KEY: misc feature

203 &lt;223&gt; OTHER INFORMATION: Incyte Clone No: 2635136

205 &lt;400&gt; SEQUENCE: 3

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206 tgcaatggcc atatgctgca gacccggagt gggtagttag ttggttaatg ccagtcttcc 60
207 tcccctggac actgagttct gctgacagcc cccgcccagc cagagctctg ctgtatacca 120
208 ccgggagtg ggtggtgtg gagcctggag gtcgcccgt gccctcctag ggctgctcca 180
209 gacagcatta aaacgctgca ggtcgcaggt gagactaaca gctgggagag ctgctccagg 240
210 catttaggac cctgactggg gcagatgagt cagcccagt ggggcagggc tcctggaacg 300
211 aggatctaca gttggagtgt cccactgtc atgtcacctg gagaaaaact ggaccaatt 360
212 cctgacagct tcattctgca accaccagtc ttccaccgg tggttcctta tgtcacgacg 420
213 atttttggag gcctgcatgc aggcaagatg gtcatgctgc aaggagtggc ccctctagat 480
214 gcacacaggt ttcaggtgga cttcagtggt ggctgcagcc tgtgtcccg gccagatatc 540
215 gccttccact tcaaccctcg cttccatacc accaagcccc atgtcatctg caacaccctg 600
216 catggtggac gctggcaaag ggaggcccgg tggccccacc tggccctgcg aagaggctcc 660

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217 agcttcctca tcctctttct cttcgggaat gaggaagtga aggtgagtgt gaatggacag 720
218 cactttctcc acttccgcta cgggctccca ctgtctcatg tggacacgct gggatatatt 780
219 ggtgacatcc tggtagaggg tgttggattc ctgaacatca atccatttgt ggagggcagc 840
220 agagagtacc cagctggaca tcctttcctg ctgatgagcc ccaggctgga ggtgccctgc 900
221 tcacatgctc ttcccagggt tctctcgctt gggcaggcca tcatagtacg gggactggtc 960
222 ttgcaagagc cgaagcattt tactgtgagc ctgagggacc aggctgcccc tgctcctgtg 1020
223 aactcagggg cctccttcgc agacagaact ctggcctgga tctcccgtcg ggggcagaag 1080
224 aaactgatct cagccccctt cctcttttac cccagagat tctttgaggt gctgctcctg 1140
225 ttccaggagg gagggctgaa gctggcgctc aatgggcagg ggctgggggc caccagcatg 1200
226 aaccagcagg ccctggagca gctgcgggag ctccggatca gtggaagtgt ccagctctac 1260
227 tgtgtccact cctgaggatg gttccaggga aataccgcca gaaaacaaga aggtcagccc 1320
228 actcccaggg cccactctc ctcccctcat taaaccatcc acctgacacc agcacatcag 1380
229 gcctgggtta cctctggggt cagcagactg agtctacagg agctttgggc ctgagggaag 1440
230 gcacaagagt gcaaaagggt ctcgaactct gcaccttctt ccaccaggag cctgggatat 1500
231 ggctccatct gccttcaggg cctggactgc actcacagag gcaagtgttg tagactaaca 1560
232 aagatactcc aaaatacaat ggcttaaaga atgtggtcat ttattcttta ttatttattt 1620
233 atttgtggtc aaataaataa ata 1643
236 <210> SEQ ID NO: 4
237 <211> LENGTH: 2290
238 <212> TYPE: DNA
239 <213> ORGANISM: Homo sapiens
241 <220> FEATURE:
242 <221> NAME/KEY: misc_feature
243 <223> OTHER INFORMATION: Incyte Clone No: 2687731
245 <400> SEQUENCE: 4
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247 agatgaagga catgccactc cgaattcatg tgctacttgg cctagctatc actacactag 120
248 tacaagctgt agataaaaaa gtggattgtc cacggttatg tacgtgtgaa atcaggcctt 180
249 ggtttacacc cagatccatt tataatggaag catctacagt ggattgtaat gatttaggtc 240
250 ttttaacttt cccagccaga ttgccagcta acacacagat tcttctccta cagactaaca 300
251 atattgcaaa aattgaatac tccacagact ttccagtaaa ccttactggc ctggatttat 360
252 ctcaaaaaca tttatcttca gtcaccaata ttaatgtaaa aaagatgcct cagctccttt 420
253 ctgtgtacct agaggaaaac aaacttactg aactgcctga aaaatgtctg tccgaactga 480
254 gcaacttaca agaactctat attaatcaca acttgcttct tacaatttca cctggagcct 540
255 ttattggcct acataatctt cttcgacttc atctcaattc aaatagattg cagatgatca 600
256 acagtaagtg gttttagtct cttccaaatc tagagattct gatgattggg gaaaatccaa 660
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263 ctagattgtc ttacattcac cccaatgat ttttcagact cccaagctg gaatcactca 1080
264 tgctgaacag caatgctctc agtgccctgt accatgttac cattgagtct ctgccaaacc 1140
265 tcaaggaaat cagcatacac agtaacccca tcagggtgta ctgtgtcatc cgttggatga 1200
266 acatgaacaa aaccaacatt cgattcatgg agccagattc actgttttgc gtggacccac 1260
267 ctgaattcca aggtcagaat gttcggcaag tgcatttcag ggacatgatg gaaatttgtc 1320
268 tccctcttat agctcctgag agctttcctt ctaactctaaa tgtagaagct gggagctatg 1380
269 tttcctttca ctgtagagct actgcagaac cacagcctga aatctactgg ataacacctt 1440

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/762,527A

DATE: 12/16/2002

TIME: 13:33:03

Input Set : A:\PF-0576 USN SEQUENCE LISTING.txt

Output Set: N:\CRF4\12162002\I762527A.raw

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L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:295 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:5